

1030

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Gately, Maurice K.
Presky, David H.

(ii) TITLE OF INVENTION: ANTIBODIES AGAINST HUMAN IL-12

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Hoffmann-La Roche Inc.
(B) STREET: 340 Kingsland Street
(C) CITY: Nutley
(D) STATE: New Jersey
(E) COUNTRY: United States
(F) ZIP: 07110-1199

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Buchholz, Briana C.
(B) REGISTRATION NUMBER: 39,123
(C) REFERENCE/DOCKET NUMBER: CD 1048P

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 973-235-6208
(B) TELEFAX: 973-235-2363

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: mouse
- (G) CELL TYPE: Hybridoma
- (H) CELL LINE: HIL-12F3-16G2

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTG GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC	48
Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser	
1 5 10 15	
CTC ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC	96
Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn	
20 25 30	
TGG ATC CGG AAA TTC CCA GGG AAT AAA TTT GAG TAC ATG GGA TTC ATA	144
Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile	
35 40 45	
AGT TAT AGT GGT AGC ACT TAC AAT AAT CCA TCT CTC AAA AAT CGA GTC	192
Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val	
50 55 60	
TCC ATC ACT CGA GAC ACA TCC AAT AAC CAG TAC TAC CTG CAG TTG AGT	240
Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser	
65 70 75 80	
TCT GTG ACT ACT GAG GAC TCA GCC ACA TAT TAC TGT GCA AGA TCT TCG	288
Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser	
85 90 95	
GAT GCT TTG GAC TAC TGG GGC GCA GGG ACC ACG	321
Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr	
100 105	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser
1 5 10 15

Leu Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn
20 25 30

Trp Ile Arg Lys Phe Pro Gly Asn Lys Phe Glu Tyr Met Gly Phe Ile
35 40 45

Ser Tyr Ser Gly Ser Thr Tyr Asn Asn Pro Ser Leu Lys Asn Arg Val
50 55 60

Ser Ile Thr Arg Asp Thr Ser Asn Asn Gln Tyr Tyr Leu Gln Leu Ser
65 70 75 80

Ser Val Thr Thr Glu Asp Ser Ala Thr Tyr Tyr Cys Ala Arg Ser Ser
85 90 95

Asp Ala Leu Asp Tyr Trp Gly Ala Gly Thr Thr
100 105

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: mouse
- (G) CELL TYPE: Hybridoma
- (H) CELL LINE: HIL-12F3-20E11

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAG GAG TCA GGA CCT AGC CTC GTG AAA CCT TCT CAG ACT CTG TCC CTC	48
Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu	
1 5 10 15	
ACC TGT TCT GTC ACT GGC GAC TCC ATC ACC AGT GGT TAC TGG AAC TGG	96
Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp	
20 25 30	
ATC CGG AAA TTC CCA GAT AAT ACA CTT GAG TAC ATG GGA TAC ATA AGT	144
Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser	
35 40 45	
TAC AGT GGT AGT ACT TAC TAC AAT CCA TCT CTC AGA AGT CGA ATC TCC	192
Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser	
50 55 60	
ATC ACT CGA GAC ACA TCC AAG AAC CAG TAC TCC ATG CAG TTG AAT TCT	240
Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser	
65 70 75 80	
GTG ACT ACT GAG GAC ACA GCC ACA TAT TAC TGT GCA AGA TCC TCG GAT	288
Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp	
85 90 95	
GCT ATG GAC TAC TGG GGC GC	308
Ala Met Asp Tyr Trp Gly	
100	

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Glu Ser Gly Pro Ser Leu Val Lys Pro Ser Gln Thr Leu Ser Leu	
1 5 10 15	
Thr Cys Ser Val Thr Gly Asp Ser Ile Thr Ser Gly Tyr Trp Asn Trp	
20 25 30	
Ile Arg Lys Phe Pro Asp Asn Thr Leu Glu Tyr Met Gly Tyr Ile Ser	
35 40 45	
Tyr Ser Gly Ser Thr Tyr Tyr Asn Pro Ser Leu Arg Ser Arg Ile Ser	
50 55 60	

Ile Thr Arg Asp Thr Ser Lys Asn Gln Tyr Ser Met Gln Leu Asn Ser
65 70 75 80

Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys Ala Arg Ser Ser Asp
85 90 95

Ala Met Asp Tyr Trp Gly
100
